



OIEP

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/998,833

DATE: 01/28/2002

TIME: 16:45:26

Input Set : N:\Crf3\RULE60\09998833.raw

Output Set: N:\CRF3\01282002\I998833.raw

1 <110> APPLICANT: THORPE, PHILIP E.  
 2 RAN, SOPHIA  
 3 <120> TITLE OF INVENTION: CANCER TREATMENT METHODS USING ANTIBODIES TO  
 4 AMINOPHOSPHOLIPIDS  
 5 <130> FILE REFERENCE: 4001.002200  
 6 <140> CURRENT APPLICATION NUMBER: 09/998,833  
 7 <141> CURRENT FILING DATE: 2001-11-30  
 9 <150> PRIOR APPLICATION NUMBER: US/09/351,543  
 10 <151> PRIOR FILING DATE: 1999-07-12  
 13 <160> NUMBER OF SEQ ID NOS: 5  
 14 <170> SOFTWARE: PatentIn Ver. 2.0  
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 17 <211> LENGTH: 2149  
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 23 aaaattttta aatttttagaa caaagctaac aaatggctag ttttctatga ttcttcttca 180  
 24 aacgctttct ttgaggggga aagagtcaaa caaacaagca gttttacctg aaataaagaa 240  
 25 ctagttttag aggtcagaag aaaggagcaa gttttgcgag aggcacggaa ggagtgtgct 300  
 26 ggcagtacaa tgacagtttt cctttccttt gctttcctcg ctgccattct gactcacata 360  
 27 ggggtgcagca atcagcgccg aagtcagaaa aacagtggga gaagatataa ccggattcaa 420  
 28 catgggcaat gtgcctacac tttcattctt ccagaacacg atggcaactg tctgtgagagt 480  
 29 acgacagacc agtacaacac aaacgctctg cagagagatg ctccacacgt ggaaccggat 540  
 30 ttctcttccc agaaacttca acatctggaa catgtgatgg aaaattatac tcagtggctg 600  
 31 caaaaacttg agaattacat tgtggaaaac atgaagtcgg agatggccca gatacagcag 660  
 32 aatgcagttc agaaccacac ggctaccatg ctggagatag gaaccagcct cctctctcag 720  
 33 actgcagagc agaccagaaa gctgacagat gttgagaccc aggtactaaa tcaaacttct 780  
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 35 cttcaacaga caaatgaaat cttgaagatc catgaaaaaa acagttttatt agaacataaa 900  
 36 atcttagaaa tggaaggaaa acacaaggaa gagttggaca ccttaaagga agagaaagag 960  
 37 aaccttcaag gcttggttac tcgtcaaaca tatataatcc aggagctgga aaagcaatta 1020  
 38 aacagagcta ccaccaacaa cagtgtcctt cagaagcagc aactggagct gatggacaca 1080  
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 40 gaggaagaga aaccatttag agactgtgca gatgtatatc aagctggttt taataaaagt 1200  
 41 ggaatctaca ctatttatat taataatatg ccagaaccca aaaaggtgtt ttgcaatatg 1260  
 42 gatgtcaatg ggggaggttg gactgtaata caacatcgtg aagatggaag tctagatttc 1320  
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 46 aagcaaaact ataggttgta tttaaaaggt cacactggga cagcaggaaa acagagcagc 1560  
 47 ctgatcttac acggtgctga tttcagcact aaagatgctg ataatgacaa ctgtatgtgc 1620

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51      ttttgaaagc gcaatgtcag aagcgattat gaaagcaaca aagaaatccg gagaagctgc 1860
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54      acaagagtct ctacttgggg tgacagtgtc cacgtggctc gactatagaa aactccactg 2040
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66      20          25          30
67      Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro
68      35          40          45
69      Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr
70      50          55          60
71      Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser
72      65          70          75          80
73      Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp
74      85          90          95
75      Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met
76      100         105         110
77      Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu
78      115         120         125
79      Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys
80      130         135         140
81      Leu Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu
82      145         150         155         160
83      Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln
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85      Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser
86      180         185         190
87      Leu Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu
88      195         200         205
89      Leu Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly Leu Val Thr
90      210         215         220
91      Arg Gln Thr Tyr Ile Ile Gln Glu Leu Glu Lys Gln Leu Asn Arg Ala
92      225         230         235         240
93      Thr Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp
94      245         250         255
95      Thr Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu
96      260         265         270
97      Lys Gly Gly Lys Arg Glu Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp

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100          290          295          300
101  Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn
102          305          310          315          320
103  Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp
104          325          330          335
105  Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser
106          340          345          350
107  Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln
108          355          360          365
109  Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg
110          370          375          380
111  Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn
112          385          390          395          400
113  Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser
114          405          410          415
115  Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn
116          420          425          430
117  Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Trp Trp
118          435          440          445
119  Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala
120          450          455          460
121  Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys
122          465          470          475          480
123  Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu
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125 Asp Phe

127 &lt;210&gt; SEQ ID NO: 3

128 &lt;211&gt; LENGTH: 2269

129 &lt;212&gt; TYPE: DNA

130 &lt;213&gt; ORGANISM: Homo sapiens

131 &lt;400&gt; SEQUENCE: 3

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134  agcaggactg ttcttccac tgcaatctga cagtttactg catgcctgga gagaacacag 180
135  cagtaaaaac caggtttgct actggaaaaa gaggaagag aagactttca ttgacggacc 240
136  cagccatggc agcgtagcag cctgcggtt cagacggcag cagctcggga ctctggacgt 300
137  gtgtttgccc tcaagtttgc taagctgctg gtttattact gaagaaagaa tgtggcagat 360
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141  tgtgcagagg gacgcgccgc tcgaatacga tgactcgggt cagaggctgc aagtgtctga 600
142  gaacatcatg gaaaacaaca ctcaagtggc aatgaagctt gagaattata tccaggacaa 660
143  catgaagaaa gaaatggtag agatacagca gaatgcagta cagaaccaga cggctgtgat 720
144  gatagaataa gggacaaacc tgttgaaaca aacagctgag caaacgcgga agttaactga 780
145  tgtggaagcc caagtattaa atcagaccac gagacttgaa cttcagctct tggaaacactc 840
146  cctctcgaca aacaaatttg aaaaacagat tttggaccag accagtgaat taaacaaatt 900
147  gcaagataag aacagtttcc tagaaaagaa ggtgctagct atggaagaca agcacatcat 960

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149   ttccatcatt gaagaactag aaaaaaaaaat agtgactgcc acggtgaata attcagttct 1080
150   tcaaaagcag caacatgatc tcatggagac agttaataac ttactgacta tgatgtccac 1140
151   atcaaactca gctaaggacc ccactgttgc taaagaagaa caaatcagct tcagagactg 1200
152   tgctgaagta ttcaaatacag gacacaccac aaatggcatc tacacgttaa cattccctaa 1260
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155   gggatttggt aacccttcag gagaatattg gctgggaaat gagtttggtt cgcaactgac 1440
156   taatcagcaa cgctatgtgc ttaaaataca ccttaaagac tgggaaggga atgaggctta 1500
157   ctcatgtgat gaacatttct atctctcaag tgaagaactc aattatagga ttcaccttaa 1560
158   aggacttaca gggacagccg gcaaaataag cagcatcagc caaccaggaa atgattttag 1620
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160   ctggttggtt gatgcatgtg gtccttccaa cttgaacgga atgtactatc cacagaggca 1740
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162   caaggccaca accatgatga tccgaccagc agatttctaa acatcccagt ccacctgagg 1860
163   aactgtctcg aactattttc aaagacttaa gcccagtga ctgaaagtca cggctgcgca 1920
164   ctgtgtcctc ttccaccaca gagggcggtg gtcggtgct gacgggaccc acatgctcca 1980
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167   gaatcagact gacagtttac agacgctgct gtcacaacca agaattgtat gtgcaagttt 2160
168   atcagtaaata aactggaaaa cagaacactt atgttatata atacagatca tcttggaaact 2220
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179             20             25             30
180   Gln Tyr Gln Val Gln His Gly Ser Cys Ser Tyr Thr Phe Leu Leu Pro
181             35             40             45
182   Glu Met Asp Asn Cys Arg Ser Ser Ser Ser Pro Tyr Val Ser Asn Ala
183             50             55             60
184   Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser Val Gln Arg Leu
185             65             70             75             80
186   Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln Trp Leu Met Lys
187             85             90             95
188   Leu Glu Asn Tyr Ile Gln Asp Asn Met Lys Lys Glu Met Val Glu Ile
189             100            105            110
190   Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile Gly
191             115            120            125
192   Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr Asp
193             130            135            140
194   Val Glu Ala Gln Val Leu Asn Gln Thr Thr Arg Leu Glu Leu Gln Leu
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196   Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys Gln Ile Leu Asp
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201               195               200               205
202   Ile Lys Glu Glu Lys Asp Gln Leu Gln Val Leu Val Ser Lys Gln Asn
203               210               215               220
204   Ser Ile Ile Glu Glu Leu Glu Lys Lys Ile Val Thr Ala Thr Val Asn
205               225               230               235               240
206   Asn Ser Val Leu Gln Lys Gln Gln His Asp Leu Met Glu Thr Val Asn
207               245               250               255
208   Asn Leu Leu Thr Met Met Ser Thr Ser Asn Ser Ala Lys Asp Pro Thr
209               260               265               270
210   Val Ala Lys Glu Glu Gln Ile Ser Phe Arg Asp Cys Ala Glu Val Phe
211               275               280               285
212   Lys Ser Gly His Thr Thr Asn Gly Ile Tyr Thr Leu Thr Phe Pro Asn
213               290               295               300
214   Ser Thr Glu Glu Ile Lys Ala Tyr Cys Asp Met Glu Ala Gly Gly Gly
215               305               310               315               320
216   Gly Trp Thr Ile Ile Gln Arg Arg Glu Asp Gly Ser Val Asp Phe Gln
217               325               330               335
218   Arg Thr Trp Lys Glu Tyr Lys Val Gly Phe Gly Asn Pro Ser Gly Glu
219               340               345               350
220   Tyr Trp Leu Gly Asn Glu Phe Val Ser Gln Leu Thr Asn Gln Gln Arg
221               355               360               365
222   Tyr Val Leu Lys Ile His Leu Lys Asp Trp Glu Gly Asn Glu Ala Tyr
223               370               375               380
224   Ser Leu Tyr Glu His Phe Tyr Leu Ser Ser Glu Glu Leu Asn Tyr Arg
225               385               390               395               400
226   Ile His Leu Lys Gly Leu Thr Gly Thr Ala Gly Lys Ile Ser Ser Ile
227               405               410               415
228   Ser Gln Pro Gly Asn Asp Phe Ser Thr Lys Asp Gly Asp Asn Asp Lys
229               420               425               430
230   Cys Ile Cys Lys Cys Ser Gln Met Leu Thr Gly Gly Trp Trp Phe Asp
231               435               440               445
232   Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Tyr Tyr Pro Gln Arg Gln
233               450               455               460
234   Asn Thr Asn Lys Phe Asn Gly Ile Lys Trp Tyr Tyr Trp Lys Gly Ser
235               465               470               475               480
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